

Sequence Alignment #2

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<!--StartFragment-->RESULT 2
TSBH_CAHFA
ID TSBH_CAHFA Reviewed; 138 AA.
AC P54828;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 24-JUL-2007, entry version 40.
DE Thyrotropin subunit beta precursor (Thyroid-stimulating hormone
DE subunit beta) (TSB-beta) (TSB-B) (Thyrotropin beta chain).
GI Name=TSBH;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
PI [1]
PP NUCLEOTIDE SEQUENCE [MFNA].
RC TISSUE=Pituitary;
RA Kania S.A., Frank L.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Indispensable for the control of thyroid structure and
CC metabolism.
CC -1- SUBUNIT: Heterodimer of a common alpha chain and a unique beta
CC chain which confers biological specificity to thyrotropin,
CC lutropin, follitropin and gonadotropin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycoprotein hormones subunit beta
CC family.
CC
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CC
DR EMBL; U51644; AAA97410.1; -, mRNA.
DR UniGene; Cfa.3841; -.
DR HSSP; P01233; IHCN.
DR Ensembl; BUSCF000000009713; Canis familiaris.
DR InterPro; IPR006200; Cys_knot.
DR InterPro; IPR002400; GF_cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR PANTHER; PT011515; Gly_hormoneB; 1.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GPCYSKNOT.
DR SMART; SM00068; GRB; 1.
DR PROSITE; PS00261; GLYC_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYC_HORMONE_BETA_2; 1.
PE 2: Evidence at transcript level;
KI Glycoprotein; Hormone; Secreted; Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 132 Thyrotropin subunit beta.
FT /FTID=FP0_0000011742.
FT PROPEP 133 138 By similarity.
FT /FTID=FP0_0000011743.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT DISULFID 22 72 By similarity.
FT DISULFID 36 87 By similarity.
FT DISULFID 39 125 By similarity.
FT DISULFID 47 103 By similarity.
FT DISULFID 51 105 By similarity.
FT DISULFID 108 115 By similarity.
SQ SEQUENCE 138 AA; 15666 MW; A3298FFDDF6A005F CRC64;

Query Match 94.5%; Score 728; DB 1; Length 138;
Best Local Similarity 94.9%; Pred. No. 5.7e-65;
Matches 131; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MTATYLMGLVFLGLACGMSFCFPTETVHVEFEKAYCLTHTTICAGYCHTDPINGKL 60
Db [|||||]:[|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 1 MTATYLMGLVFLGLACGMSFCFPTETVHVEFEKAYCLTHTTICAGYCHTDPINGKL 60
Db [|||||]:[|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 61 FLRYALSDQVCTYDFLYKTVRIIPGCPHVTYPFSYPVAVSCKGKCHNTDYSDCIHEAI 120
Db [|||||]:[|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 61 FLRYALSDQVCTYDFLYKTVRIIPGCPHVTYPFSYPVAVSCKGKCHNTDYSDCIHEAI 120
Db [|||||]:[|||||] [|||||] [|||||] [|||||] [|||||] [|||||]
Qy 121 KTHDCTKPKQSDVGVNSI 138
Db [|||]:[|||||] [|||] [|||]
Qy 121 KTHYCTFKQKSYVVGSI 138
Db [|||||]:[|||||] [|||||] [|||||] [|||||]
<!--EndFragment-->
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